IN THE SPECIFICATION:

On page 1, following the title, please insert the following paragraph:

This application is based on provisional application number 60/505,684 filed June 25, 1997 which is relied upon and hereby expressly incorporated by reference herein.

On page 12, please replace the paragraph beginning at line 10 with the following:

--DNA sequence of the PCR product used for mutation detection (SEQ ID NO:1) Oligonucleotide primers are shown by arrows and the numerals 3 and 13 (SEQ ID NOS:2 and 3). Intron sequence is shown in lower case and exon sequence in upper case. Amino acid translation of the exon is shown below the DNA sequence (SEQ ID NO:25). The circled base represents the G209A change in the mutant allele. The resulting amino acid Ala53Thr change is represented by the circled amino acid. The newly created Tsp45 I site is indicated above the DNA sequence.—

On page 15, please replace the paragraph beginning on line 1 with the following:

--Sequence of exons 1-7 of the human alpha synuclein gene, plus some flanking intronic sequence for each exon (SEQ ID NOS: 14-19). Exons 1-2 are SEQ ID NO:14, exon 3 is SEQ ID NO:15, exon 4 is SEQ ID NO:16, exon 5 is SEQ ID NO:17, exon 6 is SEQ ID NO:18 and exon 7 is SEQ ID NO:19.—

On page 32, please replace the paragraph beginning at line 22 with the following:

--DNA samples were collected upon informed consent. High molecular witht genomic DNA was isolated from whole-blood lysate by methods previously described (39). Pairwise likage analysis was performed using the MLINK program of the FASTLINK package (40-42). Allele frequencies were used as reported in the Genomic Data Base ~~(http://gdbwww.gdb.org)~~ and the Cooperative Human Linkage Consortium (CHLC) database ~~(http://www.chlc.org)~~.– Multipoint analysis was performed using the LINKMAP program of the FASTLINK package. For the multipoint analysis allele frequencies were set to 1/n where n equals the number of alleles observed. In the two point analysis LOD scores were calculated for both the reported and the 1/n allele

frequencies with minmal effect on the maximum LOD score observed. Simulations of multipoint analysis in a subset of the pedigree with different allele frequencies similarly indicated no significant effect on the scores calculated. Maximum LOD scores as shown were observed for the heterozygote and homozygote disease allele penetrance set to 0.99, which is similar to the PD allele penetrance previously reported ranging from 0.88 to 0.94 (3). All unaffected individuals used in the study were of age above the man for onset of illness. Disease allele frequency was set to 0.0001. Distances and order of genetic markers were set as reported in the CHLC database. Overlapping three point analysis was performed for markers *D4S2361, D4S1647, D4S421* and the PD locus. The 12 allele *D4S2380* locus was not included because of prohibitive time run. Multipoint analysis was performed on an IBM SP2 parallel computer and the SCI Challenge machine.—

On page 40, please replace the paragraph beginning at line 14 with the following:

--Using two primers sets designed from known database sequences (5'ATGTCTTCAAGAAGGGCTTC3' (SEQ ID NO:20); 5'CCTTGGTCTTCTCAGCTGCT3' (SEQ ID NO:21) and 5'AGCGTGGATGACCTGAAGAG3' (SEQ ID NO:22); 5'AGCACAGGTGGACAGGCCAAG3' (SEQ ID NO:23)), we have isolated two BAC clones, 139A20 and 174P13, from a Genome System commercial Bacterial Artificial Chromosome library (St. Louis, MO) which contain the human beta and gamma synuclein genes, respectively. The beta gene contained one clone 139A20 has been sequenced as shown in Figure 8 (SEQ ID ~~NO 11~~NO:11), which contains all coding exon sequences and some additional non-coding intronic sequence. The gamma clone 174P13 has been sequenced and is available in GenBank: accession number AF044311. Sequence from the 5' end is given in Figure 9 (SEQ ID ~~NO 12~~ NO:12), and the sequence from the 3' end is given in Figure 10 (SEQ ID ~~NO 13~~ NO:13). The human alpha synuclein gee has also been sequenced as shown in Figure 11, which provides the sequence of each separate exon region with some additional flanking intronic sequence for each exon (SEQ ID ~~NOs~~ NOS:14-19).--

On page 45, please delete the paragraph beginning at line 1:

~~49. This application is based on provisional application number 60/505,684 filed June 25, 1997 which is relied upon and hereby expressly incorporated by reference herein.~~

IN THE DRAWINGS:

Please substitute the attached original Figures for those that are currently present in the case.